

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 188 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of  
5 SEQ ID NOs:2, 4, 6, 8, 10, 12 and 14, or a second nucleotide sequence comprising the complement of the first nucleotide sequence.
2. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3,  
10 5, 7, 9, 11 and 13 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12 and 14.
3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are DNA.
4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are  
15 RNA.
5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.
6. An isolated host cell comprising the chimeric gene of Claim 5.
7. A host cell comprising an isolated polynucleotide of Claim 1.
- 20 8. The host cell of Claim 7 wherein the host cell is selected from the group consisting of yeast, bacteria, plant, and virus.
9. A virus comprising the isolated polynucleotide of Claim 1.
10. A polypeptide of at least 188 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group  
25 consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12 and 14.
11. A method of selecting an isolated polynucleotide that affects the level of expression of a protein involved in catabolite repression in a host cell, the method comprising the steps of:
  - (a) constructing an isolated polynucleotide comprising a nucleotide sequence of  
30 at least one of 30 contiguous nucleotides derived from an isolated polynucleotide of Claim 1;
  - (b) introducing the isolated polynucleotide into a host cell; and
  - (c) measuring the level of a polypeptide in the host cell containing the polynucleotide to provide a positive selection means.
- 35 12. The method of Claim 11 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11 and 13 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12 and 14.

13. A method of selecting an isolated polynucleotide that affects the level of expression of a protein involved in catabolite repression in a plant cell, the method comprising the steps of:

- (a) constructing an isolated polynucleotide of Claim 1;
- 5 (b) introducing the isolated polynucleotide into a plant cell; and
- (c) measuring the level of polypeptide in the plant cell containing the polynucleotide to provide a positive selection means.

14. A method of obtaining a nucleic acid fragment encoding a protein involved in catabolite repression comprising the steps of:

- 10 (a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences; and

- (b) amplifying a nucleic acid sequence using the oligonucleotide primer.

15 15. A method of obtaining a nucleic acid fragment encoding a protein involved in catabolite repression comprising the steps of:

- (a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences;

- (b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

- (c) isolating the identified DNA clone; and

- (d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

25 16. A composition comprising the isolated polynucleotide of Claim 1.

17. A composition comprising the isolated polypeptide of Claim 10.

18. An isolated polynucleotide comprising the nucleotide sequence having at least one of 30 contiguous nucleotides derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such sequences.

19. An expression cassette comprising an isolated polynucleotide of Claim 1 operably linked to a promoter.

20. A method for positive selection of a transformed cell comprising:

- (a) transforming a host cell with the chimeric gene of Claim 5 or an expression cassette of Claim 19; and

- (b) growing the transformed host cell under conditions which allow expression of the polynucleotide in an amount sufficient to complement a null mutant and alter catabolite repression pathways to provide a positive selection means.

21. The method of Claim 20 wherein the host cell is a plant cell.

22. The method of Claim 21 wherein the plant cell is a dicot or a monocot.

23. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 58 amino acids that has at least 80% identity based on the Clustal  
5 method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:16, 18, 20 and 22, or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

24. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 60% identity based on the Clustal  
10 method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 22, or a second nucleotide sequence comprising the complement of the first nucleotide sequence.